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GenCore version 5.1.6
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2, 2004, 10:27:16 ; Search time 3991 Seconds (without alignments) 10871.054 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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BD271230 Prediction of risk of interstitial lung disease. BD271230	BD271230.1 GI:33080998 JP 2002540801-A/2. Homo sapiens (human) Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9721) Duff;G.W., Giovine,F.S.D. and Whyte,M. Prediction of risk of interstitial lung disease Patent: JP 2002540801-A 2 03-DEC-2002;
RESULT 1 BD271230 LOCUS DEFINITION 1 ACCESSION 1	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE 1 AUTHORS I TITLE 5

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Stephenson, K.
Diagnostics and therapeutics for restenosis
L Patent: WO 0071753-A 16 30-NOV-2000;
Interleukin Genetics, Inc. (US)
Interleukin Genetics, Inc. (VS)
I. .9721
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
/note="IL-1B gene-'n' bases throughout the sequence A, T, C, G, other or Unknown"
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OS Homo sapiens (human)
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PD 03-DEC-2002
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PR 02-APR-1999 US 09/286108
PR 02-APR-1999 US 09/286108
PR 02-APR-1999 US 09/286108
PR 02-APR-1999 US PC 21201/68, G01N33/7088, A61K38/00, A61K45/00, A61K31/7088, A61K31/7088, A61K31/7088, A61K33/50, G01N33/53, G01N33/566, PC A61P11/00,
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1. .9721
/organism='Homo sapiens (human)'.

Location/Qualifiers
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/mol_type="genomic DNA"
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                      GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCT
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 Score 997.8; DB 6;
Pred. No. 2e-236;
0; Mismatches 2;
Query Match
Best Local Similarity 99.8%;
Matches 999; Conservative
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Hill, J.A., Wang, Z.C., Anderson, D.J. and Yunis, E.J.
Variants of il-1 beta gene and cd46 gene for diagnosing unexplained recurrent pregnancy loss
Patent: WO 0222877-A 1 21-MAR-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); DANA-FARBER CANCER INSTITUTE, INC. (US)

Location/Qualifiers
1. .9721
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                             PAT 16-JUL-2002
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                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             DNA
                            9721 bp
from Patent WO0222877.
                                                                    GI:21901721
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Best Local Similarity 99.8
Matches 999; Conservative
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unclassified.

l (bases 1 to 9721)

S Duff,G.W., Giovain,M., Barnes,P.J. and Rim,S.

Methods of diagnosing and treating chronic obstructive airway

L Patent: JP 2001522586-A 20 20-NOV-2001;

INTERLEUKIN GENETICS INC

OS Unidentified

PN JP 2001522586-A/20

PR 07-NOV-1997 GB 9723553.5,12-JAN-1998 US 09/005923 PI

GORDON W DUFF, MARKO GIOVAIN, PETER J BARNES, SIMON RIM PC

C12N15/09,C1201/68,C12N15/00

CC Strandedness: Both;

CC Methods of diagnosing and treating chronic obstructive airway

CC Methods of diseases

FH Key

I. .9721

FT source

/organism='Unidentified'.
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                         9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA
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AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA
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                                                                                 GAAATATCCTTGGCCACCGAAGACTATCCTCCTCACCCCATCCCCTTTATTTCGTTGTTCA
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/organism="unidentified"
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BD085856.1 GI:22631466
JP 2001522586-A/20.
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RESULT 6
HSIL1B
LOCUS
HOUS HUman gene for prointerleukin 1 beta.
ACCESSION X04500
VERSION X04500
VERSION X04500.1 GI:33788
KEYWORDS interleukin 1 beta.
SOURCE
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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n 2039. .2055
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2291. .2297
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                   Tree 'organism="""

"Total kindle sequence for human prointerleukin 1 beta: possible genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene with the sequence for human prointerleukin 1 alpha gene for Acids Res. 14 (20), 7897-7914 (1986)

In Station from a reverse transcribed prointerleukin 1 alpha gene for a station/Qualifiers

In Cocation/Qualifiers

Location/Qualifiers

Location/Qualifiers

In '9721

In '972
   Primates; Catarrhini; Hominidae; Homo
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4274. .4279
/note="pot.viral enhancer core sequence"
4659. .4988
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5125. .5326
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/note="pot. viral
2006. .2465
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Mammalia; Eutheria;
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AY137079
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AUTHORS
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8953
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larity 99.8%; Pred. No. 2e-236;
Conservative 0; Mismatches 2;
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Matches 999; Conser
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 17447)

S Rieder, M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A.,

Rajkumar, N.R., Toth, E.J., Yi,Q. and Nickerson, D.A.

Direct Submission

L Submitted (29-JUL-2002) Genome Sciences, University of Washington,

1705 NE Pacific, Seattle, WA 98195, USA

To cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL:

Location/Qualifiers

Light (11) 17447

Location/Qualifiers

Location/Qualifiers
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Homo sapiens interleukin 1, beta (ILIB) gene, complete cds.
AY137079
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8945 AAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGCAAAC
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8274 TITATAAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA
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                                                                                                                                    Length 17447;
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                                                                                                                                    Score 858.8; DB 9;
Pred. No. 5.5e-202;
0; Mismatches 37;
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Best Local Similarity 95.2%;
Matches 963; Conservative
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8214 AAATCAAGTC
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Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 154214)
Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lases 1 to 154214)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description of the property of the sequence of Homo sapiens BAC clone RP11-67L14

In sequence of Homo sapiens BAC clone RP11-67L14

Unpublished (2001)

I bases 1 to 154214)

S waterston, R.H.

Direct Submission

University School of Medicine, 4444 Forest Park Parkway, St. Louing Waterston, R.H.

Direct Submission

E 4 (bases 1 to 154214)

S waterston, R.H.

Direct Submission

University School of Medicine, 4444 Forest Park Parkway, St. Louing Waterston, R.H.

Direct Submission

Submitted (06-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Parkway, St. Louing Waterston, R.H.

S (bases 1 to 154214)

S (bases 1 to 154214)
GGGAGTCAGGACTGGTAGTAACAGCTACCA-TGATTTATCTATCAATGCACCAAACATCT
                                                                                                GTTGAGCAAGCGCTATGTACTAGGAGCTGGGAGTACAGAGATGAGAACAGTCACAAGTCC
                                                                                                                                                                                                                                                                                               AC079753 154214 bp DNA linear PRI 01-N
Homo sapiens BAC clone RP11-67L14 from 2, complete sequence.
AC079753
AC079753.7 GI:14318395
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

of at NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the right is RP11-725J3. Actual start this clone is at base position 1 of RP11-67L14; actual end is base position 154214 of RP11-67L14.

overlap between There are polymorphic base differences in the RP11-67L14 and RP11-725J3. Location/Qualifiers 1. .154214

FEATURES

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Length 154214;

Score 857.2; DB 9; Pred. No. 1.3e-201;

85.6%; 95.1%;

Query Match Best Local Similarity

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BD080414
Novel molecules of the Tango-77 rethereof.
BD080414
BD080414.1 GI:22626017
JP 2001512002-A/6.
Homo sapiens (human)
Homo sapiens
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    Matches 962; Conservative
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No. Homo sapiens (human)

No. 19 2001512002-A/6

PD 21-Aug-2001

PF 03-Aug-1998 JP 2000505182

PR 04-Aug-1997 US 60/054646,02-JUL-1998 US 60/091650 PI

YANG PAN

PC C12Q1/68,C07K14/52,C07K16/24,C12N5/10,C12N15/09,C12P21/02, PC C12Q1/02,

PC G01N33/15,G01N33/50,G01N33/53,G01N33/566//A61K31/ PC 7088,A61K38/00,

PC G01N33/10,A61P11/06,A61P19/02,A61P29/00,A61P37/02,C12N5/00, PC
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DNA linear PAT 27-AUG-2002 related protein family and uses
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                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176373)
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MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2001512002-A/6
PD 21-AUG-2001
PF 03-AUG-1998 JP 2000505182
PF 04-AUG-1997 US 60/054646,02-JUL-1998 US 60/09165
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CTACTCACTTAAAGCCCGGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
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Catarrhini; Hominidae;
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Human interleukin 1-beta (IL1B)
M15840
M15840.1 GI:186281
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Alu repeat; interleukin 1-beta.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Primates; Ci
1 (bases 1 to 7824)
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Catarrhini; Hominidae; Homo.
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                   135610 AAAAAA----GGTCTTTCCTGATCATTGACTTGTCTTGGATTTGACACTGAACAGTAAAG
                                                                                                                                     654 AGCAAACAGGCTGTGAGAGTTCTTGGG---ACTAAGCCCACTCCTCATTGCTGAGTGCTG
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Methods for assessing and treating leukemia Methods for assessing and treating leukemia Patent: WO 03038129-A 172 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
1. 7824
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 5.5e-196;
0; Mismatches 44;
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Sequence 172 from Patent W003038129,
AX774856
AX774856.1 GI:32486372
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Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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Best Local Similarity 94.2%;
Matches 956; Conservative
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AX774856 COCUS
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AAAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGA----CAGTAAGC
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                                                                                                                                                                  B; G00-120-094"; chromosome 2q13-q21.
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'note="interleukin-1 beta; G00-120-094"
                                 5854. .6569
/gene="ILIB"
/note="ILIB intron F; G00-120-094"
6570. .>6782
/gene="ILIB"
/note="interleukin-1 beta; G00-120-094"
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Best Local Similarity 94.2%; Pred. No. 5.5e-196;
Matches 956; Conservative 0; Mismatches 44;
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/note="Alu repeat copy B
242 bp upstream of HindIII site;
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                                                                                                                 Submitted (125-907-1987) G. Bensi, Sclavo Research Center, Siena,
11631y
Original Source text: Human DN.

Location/Qualiflars

Location
       Carinci, V., Tornese Buonamassa, D
      ugei, G., Palla, E.,
                                        eukin-1 beta gene
95-101 (1987)
      Bensi,G., Raugei,G., Palla,E
and Melli,M.
Human interleukin-1 beta gene
Gene 52 (1), 95-101 (1987)
87248099
2954882
2 (bases 1 to 7824)
Bensi,G.
Direct Submission
Submitted (26-MAY-1987) G. Be
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human STS CHLC.UTR_00699_X04500.P37183 clone UTR_00699_X04500, sequence tagged site.

G10509.

G10509.1 G1:942358

STS; STS sequence; primer; sequence tagged site.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 614)

Murray, J., Sheffield, V, Weber, J.L., Duyk, G. and Buetow, K.H.

Cooperative Human Linkage Center

Unpublished (1995)

Synonyms: UTR_00699_X04500, CHLC.UTR_00699_X04500.T36097

Contact: Dr. Jeffrey C. Murray
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                                                                                                                                                                          ACAGTCACAAGTCCCTCCTCAGATAGGAGAGGCAGCTAGTTATAAGCAGAAACAAGGTAA
                       120694 CATTGTCTGTAAAAAACCCTAGTTTTTTAATAGCTATGGAATCATTTCAATTTGGACTGG
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   TTTAATAGCTATGGAATCAATTCAATTTGGACTGG
                                                                      TGTGCTCTTTAAATCAAGTCCTTTAATTAACACTGAAAATATATAAGCTCAGATTA-T
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                                                                                                                                                         CTGAAATAAA
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Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
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Primer B: CTTGCCCCTTTGAATAAAT
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Thereof.

Novel molecules of the Tango-77 related protein family and uses
Thereof.

DO080413.1 GI:22626016

SD080413.1 GI:226016

SD080413.1 GI:22626016

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                                                                                                     TIGITIGITITGATICATIGGICTAATTIATICAAAGGGGGCAAGAAGTAG
                       TCCTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCT
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                            CCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                      ed Prepared with primer pairs derived from X04500.
Location/Qualifiers
1. .614
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180. .200
complement(389. .408)
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                                                                                                                                                                                                                                                                                                  Score 605.8; DB 11; Length 614;
Pred. No. 2.9e-139;
0; Mismatches 2; Indels 0;
         O O O
        seconds at 94 degrees
seconds at 55 degrees
seconds at 72 degrees
                                               minutes at 72 degress
                                                                 30ng genomic DNA
each 1.5 pmole
each 200 uM
0.3 units
10 ul
                                                                   Template:
Primer:
dNTPs:
Tag Polymerase:
Total Vol:
         30
75
15
27
6
                                                                                                                                        1.5mM
50mM
10mM
8.3
          denature:
annealing:
extension:
PCR cycles:
extension:
                                                                                                                                       MgCl2:
KCl:
Tris:
pH:
                                                                                                                                                                                                                                                                                                    Query Match 60.5%;
Best Local Similarity 99.7%;
Matches 607; Conservative
PCR Profile:
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486 AAATCAAGT
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primer_bind
primer_bind
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: p Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894305.
DOUNTE // BELLONGE TO THE STAND SET OF COT-2003 HOMO Sapiens interleukin 1, beta, mRNA (CDNA clone MGC:9216 IMAGE:3875593), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USAN WITH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg, R. Direct Submission Direct Submission Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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SFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFN
KIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS"
                                                                                     PRI 06-DEC-1990
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1473)
Kotenko, S. V., Bulenkov, M.T., Veiko, V.P., Epishin, S.M.,
Lomakin, I.B., Emel'yanov, A.V., Kozlov, A.P., Konusova, V.G.,
Kotov, A.Y., Kurbatova, T.V., Reshetnikov, V.L., Simbirtsev, A.S.,
Ketlinskii, S.A. and Vinetskii, Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)
2635664
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Pred. No. 5.6e-133;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58. .864
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                                                                                                                               X56087.1 GI:35662
prointerleukin 1; prointerleukin 1 beta
Homo sapiens (human)
Homo sapiens
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                                                                                     HSPROIIB 1473 bp Human mRNA for prointerleukin 1
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1. .1473
/organism="Homo sap:
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llarity 98.8%;
Conservative C
        AAAAAAAA 1510
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Matches 595; Conser
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HSPROI1B
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Best Local Similarity 99.3%; Pred. No. 6.7e-136;
Matches 605; Conservative 0; Mismatches 3;
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1263 GTTTGTTTT
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240

2, 2004, 12:34:03

Search completed: July Job time : 3999 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

(without alignments) 9284.817 Million cell updates/sec , 2004, 09:35:39 ; Search time 458 Seconds July Run on:

47-874E-2_COPY_8345_9345

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0.0. Gapext 1.0 IDENTITY Gapop 10. Scoring table:

segs, 2124099041 residues 3373863 Searched:

6747726 tisfying chosen parameters: Total number of hits sa

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution. Pred. No. is the r score greater thar and is derived by

STIMMARIES

	Description	Aaa50175 Human int	Aax75924 Human int	Abx15529 Human int	Aaa34823 Human ade	0174 Human	Aaf20945 Human int	Aac63768 Human IL-	Aac91434 Human IL-	92 Human	5639 Human	Aad51464 Human int	Aal54516 Interleuk	Acc83528 Human int	Aaa34828 Human ade	Aaf20950 Human int	Abz96644 Human nuc	Aaf21437 Human fac	Abz97131 Human enz	Aaf27666 IL-1B DNA	Aax22303 Human IL-	Aag74052 Human int	Aah24368 Human IL1	Ade84953 Farnesyl
SUMMAKIES	ΩI	AAA50175	AAX75924	ABX15529	AAA34823	AAA50174	AAF20945	AAC63768	AAC91434	AAD35192	ABZ96639	AAD51464	AAL54516	ACC83528	AAA34828	AAF20950	ABZ96644	AAF21437	ABZ97131	AAF27666	AAX22303	AAQ74052	AAH24368	ADE84953
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ALIGNMENTS

Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatoid arthritis; chronic inflammatory lung disease; antinflammatory; osteopathic; dermatological; immunosuppressive; antidiabetic; antithyroid; antiarthritic; antirheumatic; antiasthmatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds. Human interleukin-1 beta allele 2 (+6912). AAAS0175 standard; DNA; 9721 BP (first entry) 07-NOV-2000 AAA50175; RESULT 1

Location/Qualifiers
replace(8904,C)
/*tag= a
/note= "IL-1B allele 2 (+6912)" 10-FEB-2000; 2000WO-US003443 WO200047619-A1 17-AUG-2000 Key variation

sapiens

Homo

(INTE-) INTERLEUKIN GENETICS INC. Di Giovine FS; 10-FEB-1999; Duff GW,

WPI; 2000-558192/51.

Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially inflammatory diseases.

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The present sequence is that of human interleukin-1 beta (IL-IB) allele 2 (+6912), which is a form of the IL-IB gene that contains guanine at position +6912; IL-IB allele 1 (+6912) has cytosine at this position (see position +6912; IL-IB allele 1 (+6912) has cytosine at this position (see allele at marker +6912 of the IL-IB gene. The C to G transition occurs within the 3' untranslated region of the IL-IB gene and results in an increased level of IL-IB protein. Individuals homozygous for the IL-IB allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-IB protein than homozygotes for IL-IB allele 1 (+6912). Methods and kits are provided for detecting IL-IB allele 2 (+6912), or an allele in linkage disequilibrium with an IL-IB allele 2 (+6912), and thereby contermining a patient's susceptibility to developing inflammatory contermining a patient's susceptibility to developing inflammatory contermining a patient's alopecia areata, draves disease, systemic lupus in diabetes mellitus, alopecia areata, draves disease, systemic lupus cretinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, cretinopathy, periodontal disease, juvenile chronic arthritis, claimed). Identification of the IL-IB allele 2 (+6912) and its involvement in IL-IB overproduction also eables screening assays for involvement in IL-IB allele 2 (+6912). Transgenic animals are also claimed, and can be used to treat conditions associated with IL-IB allele 2 (+6912). Transgenic animals are also claimed, and can be used to candidate therapeutics
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                                                       Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection; chronic obstructive airway disease; chronic bronchitis; emphysema; asthma; chronic bronchiolitis; proinflammatory haplotype; ss.
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proinflammatory haplotype in the sample, where detection of at least one of these alleles indicates that the patient has an increased susceptibility to developing COAD. The method is useful for determining the susceptibility of subjects to developing chronic obstructive airway disease or for predicting the rapidity or ultimate progression of chronic obstructive airway disease (COAD). COAD or ultimate progression of chronic bronchitis. The method provides for early identification of chronic obstructive airway disease (COAD), facilitating administration of appropriate treatment at the earliest stage, thereby increasing the probability of a positive outcome. The present sequence represents the human IL-1B gene
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0; Mismatches 2;
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Human; ds; gene; interleukin-1B; IL-1B; chromosome 2q13; nephropathy;

W inflammatory disease; Systemic Inflammatory Response; SIRS;

Alzheimer's disease; arthritis; acute joint inflammation; opthalmopathy;

W venile chronic arthritis; asthma; bronchial asthma; pulmonary disease;

W dronic obstructive airways disease; cardiowascular disease; thyroditis;

W cardiac cell disfunction; aortic smooth muscle cell activation; trauma;

W cardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma;

W savasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;

W cardiac cell apoptosis; pastrointestinal inflammation; cerebral trauma;

W solomerulonephritis; diabetic retinopathy; drave's opthalmopathy;

W chronic lung disease; chronic sinusitis; chronic lymphocytic thyroditis;

W chronic pelvic pain syndrome; alopecia areata; Grave's disease;

W chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;

W chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;

W Hodgkin's disease; hormonal regulation; fertility; septicaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New method of determining a patient's susceptibility to inflammatory disorders - by detecting the presence of an IL-1 (44112332) haplotype, useful in designing treatment strategies that modulate the activity of proteins produced by the IL-1 gene cluster.
 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
                         9185 GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
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disease or condition. The invention allows the determination of an individual's likelihood for developing a particular disease or condition associated with interleukin 1 (IL-1) polymorphisms without necessarily determining or characterising the causative genetic variation. Diseases such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS), Alzheimer's disease, arthritis e.g. acute joint inflammatory livense control of arways disease, arthritis e.g. acute joint inflammatory juvenile control arthritis; arthritis arthridac cell disfunction e.g. aportic smooth architis; cardiowypathy and cardiac cell disfunction e.g. aortic smooth inflammators of inflammatory bowel disease, ulcerative colitis; HIV inflammatory bowel disease, ulcerative colitis; HIV inflammatory powel disease, ulcerative colitis; glabetic retinopathy, coronary artery lesions; nephropathse e.g. diabetic retinopathy, coronary corphangenticis; pulmonary diseases e.g. diabetic retinopathy, careoporosis e.g. diabetic retinopathy, careoporosis e.g. chronic lymphocytic thyroditis; chronic simusitis; thyroditis e.g. chronic lymphocytic thyroditis; chronic simusitis; thyroditis e.g. chronic prostatitis, chronic pelvic pain correcters e.g. alopecia areata, Graves disease; chronic fatigue syndrome; obesity; inflectious diseases e.g. Leprosy, inflectious diseases e.g. cerebral trauma, mycoardial disfunction; e.g. a more complasias e.g breast cancer, Hodgkin's disease; bromonal regulation e.g. fertility, septicaemia; organ transplants. This allows for a more customised approach to perventing the onset or progression of the disease customised approach to perventing the onset or progression of the disease or condition, e.g. a clinician can more effectively prescribe a therapy that will address the molecular basis of the disease or condition. Pull
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                                                                                                                                                                                                                                                                                        <u>AAAAAAAAGGGTCTCTCCTGATCATTGACTGTCTGGATTGACACTGACAGTAAGGAAAC</u>
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Disclosure, Page 673-675; 1343pp; English

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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, cytostatic and analgesic activities. The compositions are impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-conclaining ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA33312 represent the nucleotide sequences given in the sequences differ invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences given in the disclosure of the present invention. N.B. Sequences given in the disclosure of the present invention do not match lighting that corresponding SEQ ID NO: sequences given in the sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatoid arthritis; chronic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive; antiinflammatory; osteopathic; darmatological; immunosuppressive; antiinflambetic; antithyroid; antiarthritic; antirheumatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
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                                    The present sequence is that of human interleukin-1 beta (IL-1B) allele 1 (+6912), which is a form of the IL-1B gene that contains cytosine at the sosition +6912; IL-1B allele 2 (+6912) has guanine at this position (see passition +6912; IL-1B allele 2 (+6912) and the indentification of this novel allele at marker +6912 of the IL-1B gene. The C to G transition occurs cwithin the 3' untranslated region of the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B contained approximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 2 (+6912). Methods and kits are provided for detecting IL-1B allele 2 (+6912), or an allele in linkage disequilibrium with an IL-1B allele 2 (+6912), and thereby disorders, especially coronary artery disease, systemic lupus of cetermining a patient's susceptibility to developing inflammatory disorders, especially coronary artery disease, systemic lupus of cetermining a patient's alopedia areata, "uvanile chronic arthritis; peoriasis, cretinopathy, periodontal disease, juvanile chronic arthritis; peoriasis, cretinopathy, periodontal disease, juvanile chronic arthritis; claimed). Identification of the IL-1B allele 2 (+6912) and its involvement in IL-1B untagonists at can be used to treat conditions associated with IL-1B allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-1B agonists and antagonists or
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The present invanton describes low adenosate (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinilalmandory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoslobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and paripheral nervous and non-nervous system creeptors, defensins, growth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and/or pronchoonstriction) and/or lung inflammation, allergies syndrome condition selected from pulmonary vasoconstriction; inflammation, caufactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction; inflammation, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary undonery transplantation rejection, pulmonary undonery transplantation rejection, pulmonary undonery transplantation of pulmonary pulmonary transplantation of pulmonary pulmonary transplantation of pulmonary pulmonary
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                                                                                                                                                                                                                                                                                                                                      GACTGGTAGTAACAGCTACCATGATTTATCTATCAATGCACCAAACATCTGTTGAGCAAG
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                                                            The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-IRN) (+2018) allele 2, a tumour necrosis alpha (INF-A) (-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythmatosis, Sjogren's syndrome, systemic sclerosis, dermatomyocitis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease
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Gaps
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                                                                                          Unexplained recurrent pregnancy loss; immunologic reproductive failure;
URPL; prointerleukin-1beta; IL-1beta; human; ds.
                                                                                                                                                                                                                                                                                                                                                                             Evaluating risk of unexplained recurrent pregnancy loss in a subject, testing presence of a variant in interleukin-1 beta promoter region and/or in CD46 gene intron 1 region in a sample obtained from the subject.
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention and antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, a septiatory steroid in a subject, for reducing or depleting levels of of, or reducing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pot_sequences
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                                       8885 ITTATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA
                                                                                                        9005 AGGCTGTGAGAGTTCTTGGGACTAAGCCCACTCCTCATTGCTGAGTGCTGCAAGTACCTA
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interleukin-1; IL-1; gene; ds.
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reagent comprising an interactive sensor pair. The detection reagent is useful for monitoring molecular assembly events to permit the dissection of genetic and non-genetic influences on a particular biological activity. The method is useful for linking genetic variations to molecular and physiological events, drug screening, diagnostics, therapy selection and dosing, patient monitoring or environmental safety. The interactive sensor pairs may be used to screen for and identify novel agonists and antagonists or other molecules that modulate a biological activity. The method is also useful for selecting an appropriate targeted therapeutic for a subject having an infection, including viral, bacterial or fungal infection. It is also used in gene therapy. The present sequence is human interleukin-1 (IL-1) allelic gene. This sequence is used to illustrate the method of the invention
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Pred, No. 7.8e-235;
0; Mismatches 2;
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interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;
osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;
diet; nutraceutical; ds.
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The invention relates to a novel method for determining a subject's susceptibility to the early onset or progression of an ageing-related condition (EOA). The novel method comprises assessing the subject's genotype with respect to at least one allele of an interleukin (IL)-1 pattern 1, pattern 2 and/or pattern 3 (the presence or absence of at least 1 allele provides information about the subject's susceptibility to an early onset or progression of an ageing-related condition). The method is useful for determining or predicting a subject's susceptibility to the carly onset or progression of an ageing-related condition (e.g. osteoporosis, osteoarthritis, wrinkled skin, or age-related cancer) and for determining an ageing-related phenotype. The method may be a customised therapy based on the individual's genetic profile, to tailor a recommended lifestyle, including changes in exercise and diet, and to recommend nutraceuticals that are predicted to benefit a subject having a particular IL-1 genotype and EOA predisposition. This polynucleotide is sequence relating to the invention

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The present sequence is that of the interleukin-1 beta (IL-1B) gene
including the upstream promoter region. A novel function-altering
polymorphism has been discovered at position -3737 in the distal upstream
colored and including the distal upstream
colored for diagnosing an increased likelihood of developing an
increased IL-1B expression and is associated with inflammatory disease. A
claimed method of diagnosing an increased likelihood of developing an
inflammatory disease or condition associated with increased interleukin
colored in subject involves determining the identity of the -3737 IL
B allele as a type 1 (C) or type 2 (T) promoter sequence. The
inflammatory disease is especially a periodontal disease or Alzheimer's
colored inflammatory disease, action arthritis, juvenile chronic arthritis, disease, autoimmune diabetes,
insulin-dependent diabetes, diabetic periodontitis, diabetic retinopathy,
costeoarthritis, asthma, cardiovascular disease, autoimmune diabetes,
inflammatory bowel disease, ulcerative colitis, gastric ulcer, hepatic
chiflammatory bowel disease, ulcerative colitis, gastric ulcer, hepatic
colphthalmopathy, pancreatic acinitis, pulmonary disease, restenosis,
cophthalmopathy, pancreatic acinitis, pulmonary disease, restenosis,
cophthalmopathy, pancreatic acinitis, pulmonary disease, restenosis,
cophthalmopathy, pancreatic acinitis, alopecia aerata autoimmune
cophthalmopathy, pancreatic acinitis, alopecia aerata, autoimmune
cophthalmopathy, pancreatic alisease, restenosis,
cophthalmopathy, pancreatic aerate autoimmune
cophthalmopathy, pancreatic aerate autoimmune
cophthalmopathy, pancreatic aerate acinitis, alopecia aerata, autoimmune
cophthalmopathy, and disease (all claimed)
cof the -3737 IL-1B allele is also useful for determining whether a
contractic are periodor at the rage of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for preparing a composition for treating an ase or condition associated with increased interleukin nam subject, e.g. rheumatoid arthritis or ulcerative
                                                                                                                                                                                           Interleukin-1 beta, IL-1B; human; single nucleotide polymorphism; SNP; antiinflammatory; nootropic; antirheumatic; antiarthritic; cardiant; antiulcer; ophthalmological; antidiabetic; lipolytic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
replace(3870,t)
/*tag= a
/standard_name= "Single nucleotide polymorphism"
/note= "-3737 polymorphic allele 1"
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05-JUN-2002; 2002US-0386020P
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                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid, u inflammatory diseas production in a hum colitis.
                                                                                                                                                             Human interleukin-1
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                                     ACC83528 standard;
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                                                                                                                                                                                                                                                                                                                                                     Key
variation
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RESULT
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Score 997.8;

Query Match

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9e-235;
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     Pred. No. 9e-20; Mismatches
       Local Similarity 99.8
hes 999; Conservative
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AAF20950 standard; DNA; 29433

Query Match Best Local Similarity Matches 999; Conser

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Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8714 A; 6519 C; 5920 G; 8278 T; 0 U; 2 Other;
                                                                        Human adenosine receptor related polynucleotide SEQ ID NO:2517.
          29433
                                                                                                                                                                                                                                                      -US017712
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          standard;
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          AAA34828
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AAA34828
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of disease associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive currently and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The A-containing ONs break down with the carcinomas side effects. The A-containing ONs break down with the correspond to SEQ ID NO:1 to 2815, and then the last 185 convention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 convention, which correspond to SEQ ID NO:1 to 185, but the sequences differ invention, which correspond to SEQ ID NO:1 to 185, and then the last 185 convention which their correspond to SEQ ID NO:1 to 185, and then the last 185 sequences given in the disclosure of the present invention. On match the first corresponding SEQ ID NO: sequences given in the sequence of the present invention do not match is the corresponding SEQ ID NO: sequences given in the sequence of the present invention of the present invention.
Disclosure; Page 677-684; 1343pp; English
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CTCTCTCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGTTGAGCCAGGCCTCTCTCACCTCTCT
            GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAGGG
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Gaps

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Indels

1.1e-234;

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Low adenosine (A) content ant
adenosine receptors during me
and respiratory obstructions.
                                                                               24-MAR-2000; 2000WO-US008020
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J W.
             Human interleukin-
                                                                                                                                    Disclosure; Page
                                                                  WO200062736-A2
                                                                                             (UYEC-) UNIV
(NYCE/) NYCE
                                                           Homo sapiens
                                                                                       06-APR-1999;
                                                                         26-0CT-2000
      14-MAR-2001
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AAF20950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (1) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (II) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cycostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with ungivespiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, cranscription factors, immunosuppressive, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, brinding proteins, adenosine receptors, brinding proteins and malignancy associated proteins. The receptors, defensins, growth factors, vasociated proteins. The receptors, binding proteins and malignancy associated proteins and contisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy (ies) and/or undover bronchoconstriction) and/or lung inflammation, allergy (ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergy conditions, emphysemal, chronic obstructive pulmonary disease (CP), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary infections, bronchitis, pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or enecer. April 4 to AAF1843 represent human polynucleotide in the exemplification of the property of the parenty of the pare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense oligonucleotides which do not trigger
y metabolism, useful e.g. for treating cancers
                                                                                                                             human, airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
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2004, 11:27:15

7

completed: July

Search

DB

997.8;

Score

Query Match

Job time : 467 secs

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July 2, 2004, 10:39:01 ; Search time 2592 Seconds (without alignments) 11532.424 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	1	CD367424 UI-H-FT1-	CD368885 UI-H-FT1-	CD370914 UI-H-FT1-
SUMMARIES			ΙD	13 BU626628	CD367424	CD368885	CD370914
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	; %	Query	Match	59.5	59.5	59.3	59.3
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8 14 CA43151	CA307	11 13 BU62642)4 13 BU62661)6 13 BU62690	57 14 CA30598	57 14 CA44283	70 12 BQ00028	77 14 CA43153	38 14 CA30723	3 12 BQ00122	55 14 CD36778	04 14 CA44306	59 13 BU62649	38 13 BU62689	3 14 CD37052	3 12 BM99941	L7 9 AI609005	56 14 CA31001	96 13 BU62696	19 14 CA4411	73 13 BU62679	18 10 AW27308	75 14 CA43163	49 12 BG11716	11 12 BG19476	98 9 AI471571	76 14 CA3102	48 12 BM99723	54 9 AA57731	21 9 AI02236	49 9 AI56693	28 9 AI67844	14 9 AA13174	46 12 BI5197	54 14 D2073	30 14 W4710	03 9 AV7155	13 14 W3831	29 14 T29172	41 14 CD639	
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ALIGNMENTS

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                                             TTTATAAATGAGCAAATATGATACTGTTCAATGGTT
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                                                                                                                                        /organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTO-bhm-1-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dab_host="D40B" [Life Technologies]"
/lab_host="D410B (Life Technologies)"
/clone=lib="NCI_CGAP_FTO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FTO is a cDNA library constructed from a pool of BIRNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of IOwa.
TAG_IISBUB-Human Lung Aveolar Macrophage
TAG_LIB-UI-H-FTO
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Seq primer: Ml3 rc..
POLYA=Yes.
Location/Qualifiers
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Location/Qualifiers

1. 777

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/do_tsage="hault"

/do_tsage="ha
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
Homo sapiens
Homo sapiens
Homo sapiens
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 777)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Contact: Robert Straushed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 221-272, > (TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
UI-H-FT1-bjr-k-07-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bjr-k-07-0-UI 3', mRNA sequence. CD367424 GI:31151514
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="Laxon:9606"
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/dev_stage="Aveolar Macrophage"
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/lab_host="DHJ0B (Life Technologies)"
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NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_ESD_GCCCATGCCG"
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UI-H-FT1-bjx-d-03-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone
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CD368885.
CD368885.
ST.
Homo sapiens (human)

RST.
Homo sapiens (human)

RST.
Homo sapiens (human)

ROT cGAP bit.p1 /www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Contact: Robert Straved by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 221-272, >(TAAA)n#Simple_repeat
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KEYWORDS
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ORGANISM
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AUTHORS
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Location/Qualifiers

Lorganism="Homo sapiens"

/mol type="mRNA"

/mol Tribe="ul-H-FTT-bjz-j-02-0-UI"

/tissue_type="Avcolar Macrophage"

/dov stage="Adult"

/lab_host="DH10B (Life Technologies)"

/lab_host="DH10B (Life Technologies)"

/lote="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI_CGAP FTI is a normalized cDNA library constructed from a pool of #81 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6: 791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_LIB=UI-H-FTI

TAG_LIB=UI-H-FTI

TAG_LIB=UI-H-FTI
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Homo sapiens (human)

SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 618)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NALIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA sequence: 221-272, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                          CD370914
UI-H-FTI-bjz-j-02-0-UI.s1 NCI CGAP FT1 Homo sapiens CDNA clone
UI-H-FTI-bjz-j-02-0-UI 3', mRNA sequence.
CD370914
CD370914.1 GI:31155004
EST.
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CD370914/c
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GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG 60

1;

Score 593.8; DB 14; Length 618; Pred. No. 7.1e-108; 0; Mismatches 2; Indels 1;

Query Match 59.3%; Best Local Similarity 99.5%; Matches 606; Conservative (

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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Lorganism="Homo sapiens"

/ organism="Homo sapiens"

/ db xref="taxon:9606"

/ clone="UT-FT1-bhu-c-24-0-UI"

/ tissue_type="Aveolar Macrophage"

/ dev_stage="Adult"

/ lab_host="DH10B (Life Technologies)"

/ clone lib="NCI CGAP FT1"

/ note="Organ: Lung; Wector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;

NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCTATGCGC The tissue was provided by Dr. Gary W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 221-272, > (TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                      UI-H-FT1-bhu-c-24-0-UI.S1 NCI CGAP_FT1 Homo sapiens CDNA clone UI-H-FT1-bhu-c-24-0-UI 3', mRNA sequence.
CA307004
CA307004.1 GI:24470058
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 671)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
     72 TITATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGG
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TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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Location/Qualifiers

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/ organism="Homo sapiens"
// mol_type="mRNA"
// boxref="taxon:9606"
/ clone="uI-H-FrO-bhm-i-17-0-UI"
/ tissue_type="Adult"
/ lab_host="Adult"
/ lab_host="DH10B (Life Technologies)"
/ clone lib="NCI CGAP_FTO"
/ note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.

TAG_LIB=UI-H-FTO

TAG_SEQ=GGCCATGCCG"
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTO-bhm-g-02-0-UI"
/tissue_type="Alveolar Macrophage"
/dev stage="Adult"
/dev stage="Adult"
/lab_host="Digo" [Life Technologies]"
/clone_lib="NCI_GAP_FTO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of
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TAG_LIB=UI-H-FT0
TAG_SEQ=GGCCATGCCG"
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UI-H-FTO-bhm-j-10-0-UI.sl NCI_CGAP_FTO Homo sapiens CDNA clone
UI-H-FTO-bhm-j-10-0-UI 3', mRNA sequence.

BU626613.1 GI:23292828

SET.
Homo sapiens (human)

RATOCAP_FTO-PHTP-PI-M-M-M-CDI.NIM.NID-GOV/NCICGAP, Homo.

SET.
Homo sapiens (human)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL CANCET INSTITUTE, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
CONTACT: Robert Strausberg, Ph.D.
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Tissue Procurement: Robeff-Pamela, U of I
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robeff-Pamela, U of I
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remailing Procurement: Robert Strausberg, University of Iowa
DNA Sequencing by: Or. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from DNA Sequence: 221-272, > (TAAA) m#Simple_repeat
Location/Onalifiers
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Location/Qualifiers

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/mol type="mRNA"
/db zref="taxon:9606"
/clone="UI-H-FTO-bhm-j-10-0-UI"
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/clone lib="NCI CGAP FTO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not. I;
NCI CGAP FTO is a cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Pirst strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the Synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The cell line was provided by Gary W. Hunninghake from the University of lowa.

TAG_LIB=UI-H-FTO

TAG_EEQ=GGCCATGCCG"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Fukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 706)

NoT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

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Tissue Procurement: Robeff-Pamela, U of I

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Tissue Procurement: Robert Strausperg
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UI-H-FTO-bhn-h-03-0-UI.S1 NCI CGAP_FTO Homo sapiens cDNA clone
UI-H-FTO-bhn-h-03-0-UI 3', mRNA sequence.

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BU626909.1 GI:23293124
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                                                                                                                                                        CAACTGCCTGCCTTAGGGTAGTGCTAAGAGGATCTCCTGTCCATCAGCCAGGACAGTCAG
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                                                                                                      RESULT 10
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NCI CGAP_FrO is a cDNA library constructed from a pool of sI ENA samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCGATGCGG. The cell line was provided by Gary W. Hunninghake from the University of lows.

TAG_IISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FTO
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/db_xref="mcNA"

/dev_stage="Adult"

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/lab_host=="DH10B (Life Technologies)"

/location lib="NGI CGAP FTI"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

NGI CGAP FTI is a normalized cDNA library constructed from a pool of B1 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (AT)18 tail. The sequence tag for this library is GGCTTGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_INB=UI-H-FT1

TAG_INB=UI-H-FT1

TAG_INB=UI-H-FT1
                                                                                                                                                                     CA305984 170-bhs-f-05-0-UI, SI NCI CGAP_FTI Homo sapiens CDNA clone UI-H-FTI-bhs-f-05-0-UI 3', mRNA sequence.
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UI-H-DPO-avr-h-12-0-UI.81 NCI CGAP_FS1 Homo sapiens CDNA clone
UI-H-DPO-avr-h-12-0-UI 3', mRNA sequence.

UI-H-DPO-avr-h-12-0-UI 3', mRNA sequence.

CA442834.1 GI:24807254

S EST.

Homo sapiens (human)

ISM Homo sapiens (human)

ISM Homo sapiens (human)

ISM Homo sapiens (human)

ISM Mcaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CE (bases 1 to 767)

NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),

Tussue Procurement: Dr. Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLOne Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this CDNA sequence: 221-272, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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                   CTCTCTTCTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTC
                                                                                                                                                                                        CTACTCACTTAAAGCCCGCCTGACAGAAACCACGCCCACATTTGGTTCTAAGAAACCCTC
                                                                                                                                                                                                                                                                               GATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTA
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/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DPO-avr-h-12-0-UI"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP_FS1"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_FS1 a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
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TAG TISSUE=fibrosarcoma
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTCTACGAG"
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10.C
UI.H-DPD-avt.c-13-0-UI.SI NGI CGAP_FS1 Homo sapiens GDNA clone
INAGE: 5883972 3', mRNA sequence.

NAGE: 5883972 3', mRNA sequence.

BQ000281.1 GI:19725181

SET.

Homo sapiens (human)

HOMO sapiens (human)

EST.

HOMO sapiens (human)

RAMAMALIA: Primates; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SET.

HOMO Sequencia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

The formation for Mary Hendrix

CONTact: Robert Strausberg, Ph.D.

Email: cgapbs-ramanl.nih.gov

Tissue Procurement: Dr. Mary Hendrix

CONTact: Robert Strausberg, Ph.D.

Email: cgapbs-ramanl.nih.gov

Tissue Procurement: Dr. Mary Hendrix

CONTact: Robert Strausberg, Ph.D.

Email: cgapbs-ramanl.nih.gov

Tissue Procurement: Dr. M. Bento Soares, University of Iowa

CONTACT: Capabaration: Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image:lln.gov

The following repetitive elements were found in this CDNA sequence: 221-272, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=ves.
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Location/Qualifiers

1. 770

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/db_xref="taxon:9606"
/clone="InAqE:5883972"
/tissue_type="Fibrosarcema"
/lab_host="DH10B (Life Technologies)"
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CA431534 177 bp mRNA linear EST 07-NOV-2002 UI-H-FTO-bhm-o-03-0-UI.SI NCI CGAP FTO Homo sapiens cDNA clone UI-H-FTO-bhm-o-03-0-UI 3', mRNA sequence.
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                                                                                            GTTTGTTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA
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                                 CTACTCACTTAAAGCCCGCCTGACAGAAACCACGCCCACATTTGGTTCTAAGAAACCCTC
                                                                                251 GITTGTTT-ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTA
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/wol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT0"
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strong I (bases 1 to 798)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

Contact: Robert Strayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 221-272, >(TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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Location/Qualifiers

1. 798

/organism="Homo sapiens"
/mol_type="mRNA"
/db_zref="taxon:9606"
/clone="Ul-H-FT1-bhu-p-02-0-Ul"
/tissue_type="Adult"
/dab_nost="DH10B (Life Technologies)"
/dlone_tip="Not ICAP FT1"
/lab_nost="Not ICAP FT1"
/clone_lib="Not ICAP F
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TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
                                                         CA307234.1 GI:24470288
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; Not I; Not I GAP FT0 is a cDNA library constructed from a pool of a final samples from Alveolar Macrophages challenged with different treatments. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCG. The cell line was provided by Gary W. Hunninghake from the University of Iowa.

TAG_ILB=UI-H-FT0

TAG_LLB=UI-H-FT0

TAG_SEQ=GGCCATGCCG"
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IVAGE: 5892524 3', mRNA sequence.
INAGE: 5892524 3', mRNA INAGE: 589254 INIVERSITY OF IOWA CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: CHONE distribution information can be found through the I.M.A.GE. Consortium/Library Arrayed by: CHONE Soares (CHONE) Soares (CHONE) Sequence: 221-272, > (TAAA) m#Simple_repeat
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with
TITATAAATGAGCAAATATGATACTGTTCAATGGTTCTGAAATAAACTTCACTGAAGAAA
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modified polylinker, Site_I: EcoR I; Site_2: Not I;
NCI CGAP_DH1 is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGATCATTGC.
TAG_IIS=UI-H-DH1
TAG_ISE_H-H-DH1
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.larity 99.3%; Pred. No. 1.1e-107;
Conservative 0; Mismatches 3;
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17, 2003, 20:32:30 ; Search time 1145 Seconds (without alignments) 5998.482 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Murray, J., Sheffield, V, Weber, J.L., Duyk, G. and Buetow, K Cooperative Human Linkage Center Unpublished (1995) Synonyms: UTR 00699_X04500, CHLC.UTR_00699_X04500.T36097 Contact: Dr. Jeffrey C. Murray Uofi
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Location/Qualifiers
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/db_xref="taxon:9606"
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from Patent WO0039314.
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Primer B: CTTGCCCCCTTTGAATAAAT
STS size: 229
PCR Profile:
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Primer:
dNTPs:
Tag Polymerase:
Total Vol:
                                                                 The University of Iowa
Department of Pediatrics, Ior
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 656)
Kastelic, T. and Cheneval, D.
Assay for identifying compounds which affect stability of mrna
Patent: WO 0039314-A 5 06-JUL-2000;
KASTELIC TANIA (CA); CHENEVAL DOMINIQUE (CA); NOVATION
PHARMACEUTICALS INC (CA)
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SFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFN
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0; Mismatches 0;
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note="precursor protein"
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/db_xref="taxon:9606"
/map="2q12-q21"
1496 bp
Human monocyte interleukin mRNA,
M54933 M38756
M54933.1 GI:186287
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for human IL-1.
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1. .1496
/gene="IL1A"
1. .1496
/gene="IL1A"
/note="interleukin 1 m
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CDNA sequence for hume

E00846.1 GI:2169107

JP 1986119191-A/1.

unidentified.

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Human monocyte, cDNA
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87. .896
/product='human IL-1'
534. .893
/product='peptide with human IL-1 activity'
4. .710
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polyA_signal 1484. 1489.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0;
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EP 0161901.
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/db_xref="taxon:32644"
| 361 c 328 g 393
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Unknown.

Unclassified.

Unclassified.

Unclassified.

SE 1 (bases 1 to 1507)

SE Auron, P.E., Webb, A.C., Gehrke, L., Dinarello, C.A., Rosenwasser, L.J.,

Rich, A. and Wolff, S.M.

Human il-1 cDNA sequences encoding biologically-active human il-1

proteins

IAL Patent: EP 0161901-A2 1 21-NOV-1985;

Location/Qualifiers

1. 1507

/ organism="unknown"

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 9721)
Kornman, K.S., Duff, G.W., Crossman, D.C., Francis, S.E. and
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Stephenson, K.
Diagnostics and therapeutics for restenosis
Patent: WO 0071753-A 16 30-NOV-2000;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
1. .9721
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="IL-1B gene~'n' bases throughout the seq
A, T, C, G, other or Unknown"

T. 2661 a 2328 c 2122 g 2608 t 2 others
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Pred. No. 1.6e-86;
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Sequence 16 from Patent WO0071753.
AX052806
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butteryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Butter (G.W., Cox,A., Camp,N.J. and di Giovine,F.S.

Diagnostics and therapeutics for diseases associated with an il-1

inflammatory haplotype
Patent: WO 0100880-A 2 04-JAN-2001;

Interleukin Genetics, Inc. (US)

Location/Qualifiers

1. 9721

/ Organism="Homo sapiens"
/ db xref="taxon:9606"

/ UNT 2661 a 2328 c 2122 g 2608 t 2 others
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Variants of il-1 beta gene and cd46 gene for diagnosing unexplained recurrent pregnancy loss
Patent: WO 0222877-A 1 21-MAR-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; DANA-FARBER CANCER
                                                                                                                                                                                             PAT 24-JAN-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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8770 GCCTAGITITIAAIAGCIAIGGAAICAAIICAAITIGGACIGGIGIGCICICITIAAAIC
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from Patent W00100880.
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from Patent W00222877.
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Sequence 2
AX067266
AX067266.1
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AX469435.1
                              AAGTCCTTTAATT
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AX067266
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1 (Dases 1 to 9721)
Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Auron, P.E. Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene Nucleic Acids Res. 14 (20), 7897-7914 (1986)
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/note="pot. viral enhancer core sequence"
2006..2465
/number=1
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/note="direct repeat 2"
2291. .2297
/note="pot. viral enhancer core sequence"
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Location/Qualifiers
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/clone_lib="leukocyte DNA library"
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Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 194; Conservative 0; Mismatches 0;
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                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
1 2328 c 2122 g 2608
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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/note="TATA-box like s
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, INC. (US)
Location/Qualifiers
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/note="Alu repeat"
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interleukin 1 beta.
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Homo sapiens
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HSPROI1B
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prointerleukin 1; prointerleukin 1 beta.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1473)
Kotenko, S. V., Bulenkov, M. T., Veiko, V. P., Epishin, S. M.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                      8770 GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATC
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Patent: WO 0198537-A 315 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels
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Sequence 315 from Patent WO0198537.
AX419978
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1. 1473
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58. .867
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SFVQGEESNDKIPVALGLKEKNLYLSCVLKDDFRTLQLESVDPRNYPKKKMEKFFFFIFEEP
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Lomakin, I.B., Emel'yanov, A.V., Kozlov, A.P., Konusova, V.G., Kotov, A.Y., Kurbatova, T.V., Reshetnikov, V.L., Simbirtsev, A.S., Ketlinskii, S.A. and Vinetskii, Y.P. Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989) 263564
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. 353 c 325 g 387 t
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Methods, nucleotide sequences and host and endogenous protease activity
Patent: US 5861267-A 10 19-JAN-1999;
Location/Qualifiers
1. .1497
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E06734.1 GI:2174916
JP 1994041185-A/5.
Unidentified.

Synthetic construct
artificial sequences.

I (bases 1 to 1497)
Higaki,M., Shoji,Y. and Mizushima,Y.
OHOSPHOOLIGONUCLEOTIDE AND ITS USE
Patent: JP 1994041185-A 5 15-FEB-1994;
LT T KENKYUSHO: KK
PN JP 1994041185-A/5
PP 15-JUL-1992 JP 1992213519
PI HIGAKI MEGUMI, SHOJI YOKO, MIZUSHIMA YUTAKA
PC C07H21/04,A61K31/70,A61K31/70,C12P19/34;
                                                                                Length
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    /product='IL-1 beta'.
Location/Qualifiers
1. .1497
/organism="synthetic construct"
/db_xref="taxon:32630"
a 365 c 331 g 390 t
                                                                             80.1%; Score 189; DB 6; I ilarity 100.0%; Pred. No. 5.2e-84; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.2e-84;
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Oy 186 AGCAAATAT 194 |||||||| | 1451 AGCAAATAT 1459

Search completed: March 17, 2003, 21:05:13 Job time: 1157 secs

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IL-1B DNA. Uniden
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Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatoid arthritis; chronic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive; antiinflammatory; ontithyroid; antiarthritic; antirheumatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
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AAAS0174
AAA34823
AAC91434
AAD35192
AAA524828
AAA514837
AAA54822
AAA54822
AAA24822
AAA24822
AAA24822
AAA22303
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replace(8904,C)
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44
1458
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Human IL-1B gene.
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Interleukin 1-beta
Human interleukin-
Human adenosine re
                                                              ; Search time 224 Seconds (without alignments) 2372.641 Million cell updates/sec
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| SIDS2/gcgdata/geneseqn-emb1/NA1980.DAT:*
| SIDS2/gcgdata/geneseq/eneseqn-emb1/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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                                                                                                   US-09-247-874C-2_COPY_8710_8945
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Match
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Score

Result No.

10 8 4 G 6 C 8 9

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The present sequence is that of human interleukin-1 beta (IL-1B)
allele 2 (+6912), which is a form of the IL-1B gene that contains
clear aposition (see AAASO14). The linearing based on the
this position (see AAASO14). The invention is based on the
identification of this novel allele at marker +6912 of the IL-1B
clear in the C to G transition occurs within the 3 untranslated
region of the IL-1B gene and results in an increased level of IL-1B
credion of the IL-1B allele 1 (+6912). Methods and kits are
protain. Individuals homozygous for the IL-1B allele 2 (+6912)
accumulate approximately 4 times more immunoreactive IL-1B protein
than homozygotes for IL-1B allele 1 (+6912). Methods and kits are
provided for detecting IL-1B allele 2 (+6912), or an allele in
linkage disequilibrium with an IL-1B allele 2 (+6912), and
thereby determining a patient's susceptibility to developing
inflammatory disorders, especially coronary artery disease,
thereby determining a patient's susceptibility, to developing
inflammatory disorders, especially coronary artery disease,
costeoporosis, nephropathy in diabetes mellitus, alopecia areata,
graves disease, systemic lupus erythematosus, lichen sclerosis,
ulcerative colitis, diabetic retinopathy, periodontal disease,
juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
culcerative colitis, diabetic retinopathy, periodontal disease,
lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
Il-1B antegonists that can be used to treat conditions associated
with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
with IL-1B allele 2 (+6912). Transgenic animals are also claimed,
with IL-1B allele 2 (+6912). Transgenic animals are also claimed
confirm the safety and efficacy of candidate therapeutics.
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                                                                                                                                                                                                                       Novel methods and nucleic acids for diagnosing and treating disorders associated with high levels of interleukin lbeta, especially inflammatory diseases -
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                                                                                                 GENETICS INC.
                                                                                                                                                                                                                                                                                                             Claim 34; Fig 2; 74pp; English
                  US03443
                                                           99US-0247874
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Matches 236; Conserv
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This is the 3' UTR of interleukin 1-beta mRNA which contains AU-rich element (ARE) motifs. These ARE motifs are found in genes subject to mRNA instability. Identification of a compound which affects mRNA stability comprises a DNA expression system which in the absence of the test compound is capable of expressing a protein having a detectable signal. The mRNA which codes for the protein, and which is transcribed from the expression system, comprises at least one copy of a mRNA instability sequence. The mRNA is contacted with a test compound the detectable signal is measured in the presence of the test compound and compared with a control. Compounds identified by the new method can be used for the treatment of a disease or medical condition which involves inappropriate mRNA stabilization and/or accumulation and outless the protein expression (claimed) e.g. rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 TITIGATICATIGGICTAATITATICAAAGGGGGCAAGAAGTAGCAGTGICTGTAAAAGA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTAAAATGGGAATATTAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds which affect mRNA stability for the treatment disease e.g. arthritis comprises a DNA expression system expressing protein having a detectable signal
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Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels
                                                             IL-1-beta; 3' UTR; interleukin 1-beta; AU-rich element;
mRNA instability; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 656 BP; 176 A; 151 C; 129 G; 200 T; 0 other;
                                                                                                                                                                                      /rpt_type= TANDEM
/note= "3 copies of AU-rich motif"
404..408
/*tag= b
/note= "AU-rich motif"
406..414
/*tag= c
/note= "Minimal instability motif"
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 1; 31pp; English.
                            Interleukin 1-beta 3' UTR CDNA.
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(first entry)
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                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                 Homo sapiens
31-OCT-2000
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.

(I) can have respiratory, bronchodilator, antinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the cypression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, usch as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, contral nervous system (CNS) and peripheral nervous and non-nervous system creceptors, defensins, growth factors, vascactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   content antisense oligonucleotides which do not receptors during metabolism, useful e.g. for treating
                                        608
                                     AAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-1 polynucleotide fragment #2513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32-233; 1592pp; English
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atory obstructions
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                                                                                                                                                                                                                                                                                                                                          DNA; 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                   AAATGAGCAAATAT 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYEC-) UNIV EAST (NYCE/) NYCE J W.
AAF20946 standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Low adenosine (A)
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AAF20946
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condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                             1269 TTTTGATTCATTGGTCTAATTTATTCAAAGGGGCCAAGAAGTAGCAGTGTCTGTAAAAGA 1328
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                                                                                                                                                                                                                                                                                                      TTTTGATTCATTGGTCTAATTTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenosine receptor related polynucleotide SEQ ID NO:2513.
                                                                                                                                                                                                                   Query Match 82.2%; Score 194; DB 21; Length 1496; Best Local Similarity 100.0%; Pred. No. 1.3e-85; Matches 194; Conservative 0; Mismatches 0; Indels 0,
                                                                                                                                                                                  Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAATGAGCAAATAT 194
                                                                                                                                          the present invention.
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antiathmatic, cytostatic and analgesic activities. The compositions are untiathmatic, cytostatic and analgesic activities. The compositions are impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating esthme, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysems, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the conclective sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the present convention do not match up with their corresponding SEQ ID NO: sequences invention do not match up with their corresponding SEQ ID NO: sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                              16 A; 361 C; 328 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 194; DB 21;
Pred. No. 1.3e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.2%; Score 194; DE
larity 100.0%; Pred. No. 1.3
Conservative 0; Mismatches
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87..894
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1496 BP;
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Best Local 1
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AAN50060
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Rich A;
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                                                                                                                                                                                                                                                                                                                                                                                                            A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1355-1507; 482-1501; 482-677; and 1355-1507 fragments) are claimed. Also claimed is a recombinant DNA cloning vehicle contg. the human IL-1 gene sequence. Specifically the vehicle contains the sequence coding for the new 287 AA sequence (AAP50043) or the following new fragments (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-(X); (X= Asn-Ser-Ile-Trp-Thr-Gly-Val-Leu-Asn-Gln-Val-Leu).
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/product= hIL-1
/note= "N- and C-terminally truncated forms of
this sequence which retain IL-1 activity
are covered by the invention"
                                                                                                                                         Recombinant cloning vehicle contg. human interleukin-7 gene-or
fragments, producing new biologically active polypeptide(s)
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0
                                                              Rosenwasser LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine; truncated; N-terminal deletion;
                                                                                                                                                                                                                                                                                                                                          Score 194; DB 6; Length 1507;
Pred. No. 1.3e-85;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 1507 BP; 427 A; 361 C; 328 G; 391 T; 0 other;
                                                              Dinarello CA,
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                  Claim 7; Page 34-35; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ50981 standard; cDNA; 1507 BP.
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Best Local Similarity 100.0%; P:
Matches 194; Conservative 0;
                                                               Gehrke L,
           85US-0700374
                                      (NEWE ) NEW ENGLAND MED CEN
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C-terminal deletion; ss.
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P-PSDB; AAP50043.
                                                               Webb AC,
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            11-FEB-1985;
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                                                               SM;
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                                                                 Auron
Wolff
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BB90 AAATGAGCAAATAT
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12-JAN-1998;
07-NOV-1997;
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                                            Barnes PJ,
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                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                       DNA comprising part of the nucleotide sequence AAQ50981 which encodes a polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed. Specifically, the region between nucleotides 111-717 has been found to retain hIL-1 activity (see AAQ45464).
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                                                                                                                                                   :y - useful in
studying inflammation
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                                                                                                                                                                                                                                                                       Length 1507;
                                                                                                 Rosenwasser LJ;
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'onchiolitis; proinflammatory haplotype;
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                                                                                                                                                   New DNA encoding protein with IL-1 activity monitoring disease states e.g. cancer and ste.g. in arthritis etc.
                                                                                                Rich
                                                  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
(NEWE-) NEW ENGLAND MED. CENT HOSPITALS
(TUFT ) TUFTS COLLEGE.
(WELL-) WELLESLEY COLLEGE.
                                                                                                Gehrke L,
                                                                                                                                                                                       .6; 24pp; English
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        85EP-0303234.
                         84US-0611669.
85US-0700374.
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P-PSDB; AAR42213.
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                                                                                              Auron PE, Dinarel
Webb AC, Wolff SN
                                                                                                                                                                                       Claim 1; Page 11-1
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                         18-MAY-1984;
11-FEB-1985;
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The present invention describes genotyping a nucleic acid sample from a subject to determine at least one allele of an interleukin-1 (IL-1) proinflammatory haplotype. A method has also bee described for determining a subject's susceptibility to developing chronic obstructive airway disease (COAD) or for predicting the rapidity or ultimate progression of a COAD in the subject by: (a) obtaining a nucleic acid sample from the subject; and (b) detecting at least one allele of an IL-1 proinflammatory haplotype in the sample, where detection of at least one of these alleles indicates that the patient has an increased susceptibility to developing COAD. The method is useful for determining the susceptibility of subjects to developing chronic obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic bronchitis or chronic bronchiolitis. The method provides for early identification of chronic obstructive airway disease (COAD), facilitating administration of appropriate treatment at the earliest stage, thereby increasing the probability of a positive outcome. The present sequence represents the human IL-1B gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease
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                                                                                                                                                                                                                                                                                                                                                                           Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory haplotype alleles, useful for predicting susceptibility to developing chronic obstructive airway or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 2; 37pp; English
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98US-0005923
97GB-0023553
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cartivating peptide factors and malignancies, such as stimulating and activities and antibodies, antibody receptors, cytokines and chemokines, endosenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, contral creceptors, and peripheral nervous and non-nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction and/or lung inflammation, and/or surfactant hypoproduction which are associated proteins. The and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergie (RDB), pain, cystic fibrosis (CP), allergie (RDB), pain, cystic fibrosis (CP), allergie (CDB), pulmonary infections, bronchitis, and antisone election, pulmonary infections, bronchitis, and or rejection, pulmonary infections, the present description or antisense oliconer, and or rejection, pulmonary infections, and or rejection, including respirato
s syndrome; pain; cystic fibrosis; allergic rhinitis; lon; emphysema; pulmonary transplantation rejection; pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          content antisense oligonucleotides which do not receptors during metabolism, useful e.g. for treating
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cancers and respir
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                                                                                                                                                                WO200062736-A2
                                                                                                                                                                                                                                                       24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                               (UYEC-) UNIV
(NYCE/) NYCE
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                       06-APR-1999;
                                                                                                                                                                                                            26-OCT-2000
                                                                        cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                    Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8710
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The present sequence is provided in a specification relating to a method for determining whether a subject has or is predisposed to develop an interstitial lung disease. The method involves detecting an interleukin-1 receptor antagonist (IL-1RN) (+2018) allele 2, a tumour necrosis alpha (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with either of these two alleles. The method may be used to determine whether a subject has or is predisposed to develop an interstitial pneumonia or a pulmonary fibrosis and other disorders such as rheumatoid arthritis, systemic lupus erythmatosis, Sjogren's syndrome, systemic sclerosis, dermatomyocitis. The method is also used for identifying molecules which can be used as therapeutics for treating interstitial lung disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8829
8830 AGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTAAATGGGAATATTAT 8889
                                                                                                                                                                                                                                                                                                                                     Human, IL-1B; interleukin-1B; cytostatic; antiinflammatory; immunosuppressive; dermatological; antimicrobial; antiarthritic; IL-1 receptor antagonist; tumour necrosis factor alpha antagonist interstitial lung disease; interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis; systemic lupus erythmatosis; Sjogren's syndrome; systemic sclerosis; dermatomyocitis; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8710 ritrgarrcarregicraarrrarrcaaaegegecaagaagraecaerereraaaaaa 8769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for predicting the risk of interstitial lung disease, compadetecting an interleukin-1 receptor antagonist allele and tumor necrosis alpha allele or an allele in linkage disequilibrium with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8770 GCCTAGTITITAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTTAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whyte M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENETICS INC.
                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 2; 102pp; English
                                                                                                                                                                                          standard; DNA; 9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-US08492.
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                                                                                                8903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           either of these alleles
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                                                            181 AAATGAGCAAATAT
                                                                                             AAATGAGCAAATAT
                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                      Human IL-1B
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The present sequence is that of human interleukin-1 beta (IL-1B) allele 1 (+6912), which is a form of the IL-1B gene that contains cytosine at position +6912; IL-1B allele 2 (+6912) has guanine at this position (see AA50175). The invention is based on the identification of this novel allele at marker +6912 of the IL-1B gene. The C to G transition occurs within the 3' untranslated cegion of the IL-1B gene and results in an increased level of IL-1B protein. Individuals homozygous for the IL-1B allele 2 (+6912) accumulate approximately 4 times more immunoreactive IL-1B protein than homozygotes for IL-1B allele 1 (+6912). Methods and kits are provided for detecting IL-1B allele 2 (+6912), or an allele in linkage disequilibrium with an IL-1B allele 2 (+6912), and thereby determining a patient's susceptibility to developing inflammatory disease,
                           8888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
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                                                                                                                                                                                                                                                                              Interleukin-1 beta; IL-1B; human; polymorphism; inflammation; coronary artery disease; osteoporosis; nephropathy; alopecia areata; Graves disease; systemic lupus erythematosus; lichen sclerosis; ulcerative colitis; diabetic retinopathy; periodontal disease; juvenile chronic arthritis; psoriasis; insulin dependent diabetes; asthma; lung fibrosis; chronic inflammatory liver disease; rheumatoid arthritis; chronic inflammatory lung disease; antiinflammatory; osteopathic; dermatological; immunosuppressive; antidiabetic; antithyroid; antiarthritic; antitheumatic; antiasthmatic; antipsoriatic; hepatotropic; antiulcer; diagnosis; therapy; ds.
              AAGACTGAAAATATATAAGCTCAGATTATTAAATGGGAATATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids for diagnosing and treating (igh levels of interleukin lbeta, especially ases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
replace(8904,G)
/*tag= a
/note= "IL-1B allele 1 (+6912)
                                                                                                                                                                                                                                                       beta allele 1 (+6912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC.
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                                                                                                                                                                 BP
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                                                                                                                                                               DNA; 9721
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                                                                                                                                                                                                                            entry)
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                                                                                      8903
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                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                        Human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel methods and associated with hi inflammatory disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-558192/5
                                                          AAATGAGCAAATA
                                                                                     AAATGAGCAAATA
 AAGTCCTTTAATT
                            8830 AAGTCCTTTAATT
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variation
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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8829
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Graves disease, systemic lupus erythematosus, lichen sclerosis, Graves disease, systemic lupus erythematosus, lichen sclerosis, ulcerative colitis, diabetic retinopathy, periodontal disease, juvenile chronic arthritis, psoriasis, insulin dependent diabetes, asthma, chronic inflammatory liver disease, chronic inflammatory lung disease, lung fibrosis, and rheumatoid arthritis (claimed). Identification of the IL-IB allele 2 (+6912) and its involvement in IL-IB averproduction also eables screening assays for identifying IL-IB antagonists that can be used to treat conditions associated with IL-IB allele 2 (+6912). Transgenic animals are also claimed, and can be used to identify IL-IB agonists and antagonists, or to confirm the safety and efficacy of candidate therapeutics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITIGATICATIGGICTAATITATICAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels
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antisense oligonuclectide (ON) with low adenosition comprising an artisense oligonuclectide (ON) with low adenosition (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic.

C antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary ceffects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, emphysema, chronic obstructive (ibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (OCDD), and cancers such as leukaemias, lucluding breast and prostate cancers which may metastasise to the lungs, including broast and prostate cancer. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. APA32313 to APA35312 represent the invention, which correspond to SEQ ID NO:1 to 2815, and then the last (SAA32223 to APA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences

C invention do not match up with their corresponding SEQ ID NO: sequences
     ma, respiratory distress syndrome, ischemia or
                                                                       '3-675; 1343pp; English
                                                                      67
   emphyse
                                                                       Page
                                                                      Disclosure;
bronchitis,
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Determining whether a subject has or is predisposed to disease associated with IL-1 polymorphism involves determining presence marker or allele comprising IL-1 inflammatory haplotype

Disclosure; Fig 4; 84pp; English.

Di Giovine FS;

Camp NJ,

Ą, Cox

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WPI; 2001-102903/11.

(INTE-) INTERLEUKIN GENETICS INC

99US-0345217.

30-JUN-1999;

Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;

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                                                                                                                   GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTTTTTAAATC 120
                                 0; Gaps
                                                                                                                                                                         AAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTAT
                                                                                                                                     GCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTTTTAAATC
                                                                                                                                                                                                     AAGTCCTTTAATTAAGACTGAAATATATAAGCTCAGATTATTTAAATGGGAATATTAT
Query Match 82.2%; Score 194; DB 21; Length 9721; Best Local Similarity 100.0%; Pred. No. 1.3e-85; Matches 194; Conservative 0; Mismatches 0; Indels 0;
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inflammation; infection;
                DNA; 9721
                                                (first
                AAF27666 standard;
                                                                              IL-1; interleukin;
                                                                                              Unidentified
                                               02-APR-2001
                                                               IL-1B DNA
                               AAF27666,
RESULT 12
AAF27666
ID AAF2
XX
AC AAF2
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DT 02-P
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DE IL-1
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PN WO2C
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30-JUN-2000; 2000WO-

WO200100880-A2

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                                                                                                                                                                                                                                                                     The present invention relates to a new method for determining whether a subject has or is predisposed to developing a disease or condition that is associated with an IL (interleukin)-1 inflammatory haplotype, comprises detecting at least one allele of the haplotype, where the presence of the allele indicates that the subject is predisposed to the development or has the disease or condition. The method is useful for determining whether a subject has or is predisposed to inflammatory disease, a degenerative disease, an immunological disorder, an infectious disease, trauma induced disease, or cancer. The above conditions associated with an IL-1 inflammatory haplotype can be treated or prevented by administering a therapeutic that compensates for a causative mutation that is in linkage diseaulibrium with at least one IL-1 polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.2%; Score 194; DB 22; Length 9 Best Local Similarity 100.0%; Pred. No. 1.3e-85; Matches 194; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is given in a specification relating to a method for determining whether a subject has or is predisposed to developing an arterial restenosis. The method comprises detecting a restenosis associated allele (RAA) in a nucleic acid sample from the subject, where detection of the RAA indicates that the subject has or is predisposed to the development of a restenosis. The restenosis associated allelic pattern permits the diagnosis of occlusive cardiovascular disorder. The diagnosis allows the most suitable treatment methods for restenosis to be used e.g. selecting therapies for initial vascular stenosis most likely to avoid subsequent stenoses. The detection methods identify restenosis therapeutics, agonists and antagonists, (proteins, peptides, e.g. anti-sense, ribozyme and triplex nucleic acids) which are used to treat restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ent pregnancy loss; immunologic reproductive failure; in-lbeta; IL-lbeta; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA
                                                                                                                                                                                                                                                                         Diagnosing or determining susceptibility to developing restenosi
involves detecting restenosis associated allele in a nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.2%; Score 194; DB 22; Length 9721; ilarity 100.0%; Pred. No. 1.3e-85; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                   Stephenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                 Francis SE,
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                                                                                                                                                                                Crossman DC,
                                                                                                                                                                                                                                                                                                                                                                  129pp; English.
                                                                                                                                      (INTE-) INTERLEUKIN GENETICS
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                                                                 JS-0317674.
JS-0431352.
                     24-MAY-2000; 2000WO-US14299
                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is ydetermining whether a subsarterial restenosis. The interest allele (RAA) in the second se
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                                                                                                                                                                                GW,
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Best Local Similarity
Matches 194; Conser
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2;
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                                                                 24-MAY-1999;
01-NOV-1999;
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                                                                                                                                                                                 Kornman KS,
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Low adenosine antisense oligonucleotide; phosphorothicate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8769
                                                                                                                                                                                                                              Evaluating risk of unexplained recurrent pregnancy loss in a subject, by testing presence of a variant in interleukin-1 beta promoter region and/or in CD46 gene intron 1 region in a sample obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for evaluating and treating risk of unexplained recurrent pregnancy loss (URPL) in a subject suspected of having immunologic reproductive failure. The method involves testing a sample obtained from the subject for the presence of a variant in the human interleukin-lbeta (IL-lbeta) promoter region, and/or a variant in the CD46 gene intron 1 region, where the presence of the variant, indicates an elevated risk of developing recurrent pregnancy loss. The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Pred. No. 1.3e-85; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        Example 2 and 3; Page 51-54; 57pp; English
                                                                                                                               Anderson DJ, Yunis
                                                (BGHM ) BRIGHAM & WOMENS HOSPITAL II
(DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
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12-SEP-2000; 2000US-231785P
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                                                                                                                                                                                    WPI; 2002-362362/39
                                                                                                                             Hill JA, Wang ZC,
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Best Local Simi
Matches 194;
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99US-0127958

EAST CAROLINA J W.

us-09-247-874c-2_8710_8945.oli.rng

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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                      Disclosure; Page 221-227; 1592pp; English
                         24-MAR-2000; 2000WO-US08020
                                                                       WPI; 2000-679539/66
     WO200062736-A2
                                             (UYEC-) UNIV
(NYCE/) NYCE
                                    06-APR-1999;
              26-OCT-2000
                                                             Nyce JW;
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and cativating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific endomes, chemokine receptors, adenosine receptors, bradykinin receptors, central or nervous system (CNS) and peripheral nervous and non-nervous system companies, growth factors, bradykinin receptors, central cransmitters, defensins, growth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypotroduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiratory vasoconstriction, inflammation, callergies, asthma, impeded respiratory vasoconstrictions, bypertension, emphysema, chronic obstructive pulmonary disease (CPD), hypertension, emphysema, chronic obstructive pulmonary disease (CPD), hypertension, emphysema, chronic obstructive pulmonary vieterions. ntation rejection, pulmonary infections, bronchitis, 18434 to AAF21543 represent human polynucleotide sense oligonucleotides used in the exemplification of 0; Gaps Query Match 82.2%; Score 194; DB 21; Length 29433; Best Local Similarity 100.0%; Pred. No. 1.2e-85; Matches 194; Conservative 0; Mismatches 0; Indels 0; 8714 A; 6519 C; 5920 G; 8278 T; 2 other; the present invention allergies, asthma, in (RDS), pain, cystic f hypertension, emphyse pulmonary transplants and/or cancer. AAF184 fragments and antiser Sequence 29433 BP;

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TTTTGATTCATTGGTCTAATTTATTCAAAGGGGCAAGAAGTAGCAGTGTCTGTAAAAGA 22236 GCCTAGTTTTTAATAGCTATGGAATCAATTTGGACTGGTGTGCTCTTTTAATC 120 GCCTAGTTTTTAA 22237 22177 61 d d 8

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Search completed: March 17, 2003, 20:46:15 Job time : 257 secs

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AA923615 nq98b03.s
W38319 zc77b02.s1
AA131744 z135f02.s
AI022364 ow64g05.x
AI678441 tu82d01.x
BM997237 UI-H-DH0-
                                                                                  March 17, 2003, 20:34:55; Search time 1462 Seconds (without alignments) 2614.319 Million cell updates/sec
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AAS77318 AWS77318 BQ001221 BQ001221 BQ000281 A1609005 BG194765 A1566931 BE19707 AA382165 BG19263 AA471571 T29172 AA362146 BG117168 D20737 AA362170 AA362067 C06317 BE183186 BE19601 AWY79422 BG058513 BE183137 AA715551 AA916006 BH598295 AG163910 CNS060CR C53301 AZ236878 BH598295 AG163910 CNS060CR C53301 AA715551 AA916066 BH598295 AG163473 BG148984 BM864065 BH674814 AA436473 BG809864 AV702246	324 bp m 324 bp m 3330 INTERLEUKIN-1 Bi 5330 INTERLEUKIN-1 Bi 534) 54) 54) 55 56 57 59 54 57 59 50 50 50 50 50 50 50 50 50
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88 98 98 98 98 98 98 98 98 98 98 98 98 9	AA923615 AA923615 Sequence. AA923615 AA923615 AA923615 AA923615 Homo sapiens Evaryota; Metazoa; Chordata; Crē Mammalia; Eutheria; Primates; Cat 1 (bases 1 to 324) NCI-CGAP http://www.ncbi.nlm.nih. NATional Cancer Institute, Cancer Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Ilan Kirsch, Ph.D. cDNA Library Arrayed by: Greg Le CDNA Library Arrayed by: Greg Le CONA Library Arrayed by: Greg Le CONE CONE GISTAND CONE CONE GISTAND CONE MWW-bio.llnl.gov/brp/image/image
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 413)

Killier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Rucaba, T., Lacy, M., Le, M., Mardis, E., Moore, S., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Scares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Watterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags you so you had an all so to the second the second that the second the second that the second the second that the second that the second that the second the second the second the second that second the second the second that second the second the second the second that second the second the second that the second the second the second that the second the second that the second th
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 -40m13 fwd. ET from Amersham
                  ity sequence stop: 214.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 514)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Merck EST Project

L Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 277.
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2135f02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:503931 3' similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.
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Pred. No. 7.2e-93;
0; Mismatches 0;
Seq primer: mob.REGA+ET
High quality sequence stop: 3
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; P. Matches 189; Conservative 0;
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AA131744.1 GI:1693270
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/db_xref="GDB:3808919"
/db_xref="taxon:9606"
/clone="INAGE:503931"
/clone lib="Soares_pregnant_uterus_NbHPU"
/clone lib="Soares_pregnant_uterus_NbHPU"
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/dev_stage="adult"
/lab_host="DH103"
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/note="Organ: uterus; Vector: pT7T3-Pac; Not I;
/note="Organ: uterus; Vector: pT7T3-Pac; Not I;
/note="Organ: uterus; Vector: pT7T3-Pac; Not I;
/note="Organ: uterus; Not I;
/note="Organ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 521)

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1077 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 403.

Location/Qualifiers

1. 521

/organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone="IMAGE:1651640"
/clone="IMAGE:1651640"
/clone="IMAGE:1651640"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521 bp mRNA linear EST 28-AUG-1998 clone IMAGE: 1651640 3' similar to gb: M15330 INTERLEUKIN-1 BETA A1022364
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AI022364.1
EST.
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AI022364/c
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DEFINITION
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AUTHORS
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Endanguels Eutheria; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

2 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

2 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

2 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

2 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

2 Unpublished (1997)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-r@mail.nih.gov

2 Email: cgapbs-r@mail.nih.gov

3 Email: cgapbs-r@mail.nih.gov

4 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.

5 CDNA Library Preparation: Life Technologies, Inc.

5 CDNA Library Arrayed by: Greg Lennon, Ph.D.

6 CDNA Library Arrayed by: Greg Lennon, Ph.D.

6 CDNA Library Arrayed by: Greg Lennon, Ph.D.

7 COne distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

8 Www-bio.llnl.gov/bbrp/image/image.html

8 Insert Length: 1763 Std Error: 0.00

8 Seg primer: -40UP from Gibco

8 High quality sequence stop: 404.
A1678441 528 bp mRNA linear EST 15-DEC-1999 tu82d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2257537 3' similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.
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/clone_lib="NCI_CGAP_Gas4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                                                                                  173
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Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0;
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A1678441.1
EST.
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AGCAAATAT 44
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A167841/c
LOCUS
DEFINITION
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COMMENT
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AGCAAATAT
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Best Local (
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AA577318/c
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ORIGIN
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VERSION
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AUTHORS
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="NCI CGAP_DH0"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_DH0 is a cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo,
                                                                                                                                         ö
signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
                                                                                                                                                                             GITITITAATAGCIATGGAATCAATITCAATITGGACTGGTGTGCTCTCTTTAAATCAAGTC 108
                                                                                                                                                                                                             TGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTC 125
                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                GAAAATATATAAGCTCAGATTATTTAAATGGGAATATTTATAAATG
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                                                                                                                Length 528;
                                                                                                                                        Indels
                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0;
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                                                                              98 C.
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AGCAAATAT 39
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BM997237/c
LOCUS
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                                                                               BASE COUNT
ORIGIN
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AUTHORS
TITLE
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COMMENT
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Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG LIB=UI-H-DH0

TAG LIB=UI-H-DH0

TAG TISSUE=lung

TAG SEQ=AGATCATTGC"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1351 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 414.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 554)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,

Ph.D.
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100.0%; Pred. No. 7.5e-93;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1075382"
/clone_lib="NCI_CGAP_CO9"
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AA577318.1
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137 g
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BQ001221.1 GI:19726121
                                                                                                                                                           80.1%;
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Best Local Similarity 100.
Matches 189; Conservative
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image/image.html
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/note="Corgan: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from modified polylinker; lst strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 bp mRNA linear EST 03-JAN-2000
NCI CGAP CO14 Homo sapiens CDNA clone IMAGE:2801425 3'
gb:MI5330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
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Catarrhini, Hominidae, Homo.
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0
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                                                                                                                                                                                                  others
                                                                                                                                                                                                                                              80.1%; Score 189; DB 9; Length 55
100.0%; Pred. No. 7.5e-93;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: polyT not found Seq primer: -40UP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
1. .618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone="IMAGE:2801425"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 618)
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xu27h01.x1 ]
similar to
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Best Local Similarity
Matches 189; Conser
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AW273081.1
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COMMENT
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 703)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 221-272, > (TAAA) n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
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Homo sapiens cDNA clone
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/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed
/tissue_type="moderately-differentiated adenocarcinoma"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1,7 kb. Life Technologies catalog #:
11531-019"
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0
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1. 703

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI_CGAP_DHI"
/tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                               Indels
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O
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; Pred. No. 7.6e-93;
0; Mismatches 0;
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UI-H-DH1-awp-g-21-0-UI.s1 NCI_CGAP_DH1 I
IMAGE:5892524 3', mRNA sequence.
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according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG_LIB=UI-H-DH1

TAG_LIB=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1

TAG_LIS=UI-H-DH1
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Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 770)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Library M. M. M. Bento Soares, University of Iowa DNA Library M. M. M. Bento Soares, University of Iowa DNA Library M. M. M. M. Bento Soares M. M. M. M.
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UI-H-DP0-avt-c-13-0-UI.s1 NCI_CGAP_Fs1 Homo sapiens cDNA clone
IMAGE:5883972 3', mRNA sequence.
BQ000281
BQ000281.1 GI:19725181
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5883972"
/clone_lib="NCI_CGAP_Fs1"
/tissue_type="Fibrosarcoma"
/lab_host="DH10B_(Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.1%; Score 189; DB 14; Best Local Similarity 100.0%; Pred. No. 7.7e-93; Matches 189; Conservative 0; Mismatches 0;
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1. .770
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/note="Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_FSI is a cDNA library containing the following tissue(s): Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 817)

I (bases 1 to 817)

NoI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library is GTTCTACGAG.
TAG_LIB=UI-H-DP0
TAG_TISSUE=fibrosarcoma
TAG_SEQ=GTTCTACGAG"
a 148 c 177 g 224
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AI609005.1 GI:4618172
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Best Local Similarity 100.
Matches 189; Conservative
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AI609005/c
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Matches 189; Conserv
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ESM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 911)

R Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,

Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, S., Leventhal, J., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of gene expression

Activation of gene expression

activation of gene expression

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9590

Fax: 216 361 9590
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63
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hersys RAGE Library Homo sapiens cDNA,
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Pred. No. 7.9e-93;
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163 c 187 g 231 t
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100.0%; Pre
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RST14064 Ath
BG194765
BG194765.1
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Matches 189; Conser
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BG194765/C
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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 549)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, En.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1104

Std Error: 0.00
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone lib="Athersys RAGE Library"
/cell line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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tq67h02.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2213907 3'
similar to gb:MIS330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 170
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/db_xref="taxon:9606"
/clone="IMAGE:2213907"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 0
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
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High quality sequence stop:
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differentiated (4 pooled tumors, including primary and metastatic) "
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and aco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
73 a 107 c 119 g 149 t lothers
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SM Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 746)

SS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Capabs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11530 row: g column: 07

High quality sequence start: 3

High quality sequence start: 3

High quality sequence stop: 740.

Location/Qualifiers

1.746
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NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211294 3',
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stroyed); RNA source leukocytes from anonymous pool of
-activated adult donors. Library is oligo-dT primed
directionally cloned (EcoRV site is destroyed upon
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5211294"
/clone="lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
/note="Vector: pCMV-SPORT6
(destroyed); RNA source le
non-activated adult donor
and directionally cloned
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603061928T1 NIH
mRNA sequence.
BIS19707
BIS19707.1 GI:
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Best Local Similarity
Matches 147; Conserv
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BI519707/c
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DEFINITION
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/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ clone=lib="NCI CGAP_FS1"
/ tissue type="Fibrosarcoma"
/ tissue type="Fibrosarcoma"
/ lab_host="DH10B (Life Technologies)"
/ lab_host="DH10B (Life Technologies)"
/ lab_host="DH10B (Life Technologies)"
/ lab_host="Uector: pT773-Pac (Pharmacia) with a modified
polylinker; Site=1: EcoR I; Site=2: Not I; NCI CGAP_FS1 is a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATC number CCL-121). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

U Uppublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 219-270, > (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UI-H-DPO-avf-1-11-0-UI.s1 NCI_CGAP_FS1 Homo sapiens cDNA clone IMAGE:5878810 3', mRNA sequence.
BM999417.1 GI:197243'A
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cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 ATTCATTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTA 89
                                                                                                                                                                                                                                                 Length 746;
                                                                                                                                                                                                                                                 62.3%; Score 147; DB 13; Length 7 ilarity 100.0%; Pred. No. 9.5e-70; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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AUTHORS
TITLE
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a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTCTACGAG.

TAG_LIB=UI-H-DP0

TAG_TISSUE=fibrosarcoma

TAG_SEQ=GTTCTACGAG"

a 154 c 181 g 231 t 3 others
                                                                                                                                                                                                  0; Gaps
                                                                                                      Length 793;
                                                                                                        Query Match 60.6%; Score 143; DB 14; Length 79 Best Local Similarity 100.0%; Pred. No. 1.5e-67; Matches 143; Conservative 0; Mismatches 0; Indels
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Search completed: March Job time : 1464 secs

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